GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT GTTGAAGGGTGTTTTTTTTTTTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA CTACTCTCTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG CTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT ATGATGATGATGAGGACAACTCTCTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTCCA TTTGATCTGTTTCCAATGTGŢCCATTTGGATGTCAGTGCTATTCACGAGTTGTACATTGCTC AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT CTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCACAAAGAA GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAA GGAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA GCCAGGGGCATTTGAAGGGGTGACGGTGTTCCATATCAGAATTGCAGAAGCAAAACTGACCT CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA ACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT TGGAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG AAATGCAACCTGCAACATTTCGTTGTGTTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACTTT $\texttt{GGAATG} \underline{\textbf{TAA}} \texttt{TAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAAATCCCTACATT}$ AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGAT CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAAGTAAGATATTCGGTA TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT TAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT ${\tt GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT}$ CATCTTAAAGTATGATTTGATATATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT CTTTATGTTTAAAACTAATTTCTTAAAATAAAGCCTTCAGTAAATGTTCATTACCAACTTGA ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACTCGCATTTT AATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC CACTAACAATTCTACACCAAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

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<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

CGGACGCGTGGGCGGGCCCGCSGCACCGCCCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC CTCCCTCCGCCCGCTCCCGCGCCCTCCCTCCCTCCCCAGCTGTCCCGTTCGCGTCATGCCGAGCCTCCC GGCCCGCCGGCCCGCTGCTGCTCCTCGGGCTGCTGCTCGGCTCCCGGCCGGCCCGGCCCGGCCCAGA GCCCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGCTGCACCTTCGGCGG GAAGGTCTATGCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTCGGGGTGATGCGCTGCTGTG CGCCTGCGAGGCGCCTCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACCAGA GTGCCCAACCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG CAGTTCGGAGCGGCAGCCGAGCCGTCCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG CGGGGAGCCAGGCGCTGAGGAGCGGCCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGCCCGAG GTCGCAGGCGGTGCACGAGCCCGAGTCTCGCTGCTGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCT AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA TGTGGCACTTGTGACACTCACCCTTCAGGGGAGGTCTGGGGGGCCTCTCATCCGGCACCGGGCCCTGGCTGC AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCCACAGCAGGGGGGTAGGGGGCATCACCTGCTCACTCT CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCA GATGGCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT GGCCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCCTGAACGT GGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCACGTGGCTGCCCTACTGTGGGCATAGCGCCCG CTGGCTTTCCTTGGATACCCACTGTCACCTGCACTATGAAGTGCTGCTGGCTTGGTGGCTCAGAACAAGG AGAGGCCCAGGGTGTGGAGGACCTGGAGCCGGAACTGCTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCAAACCTGGTGGTCCTGGGCGGCCCCGAGACCCCAACACATG CGACCAGTGCTGCCCTGTTTGCCCTGAGAAACAAGATGTCAGAGACTTGCCAGGGCTGCCAAGGAGCCGGGACCC AGGAGAGGCTGCTATTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCC TCCCCGGCTGGCCTGTGCCCAGCCTGTGCGTGTCAACCCCACCGACTGCTGCAAACAGTGTCCAGTGGGGTCGGG GGCCCACCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCC AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTC GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT GCATTCTCCTGTGGGAAGCCCAGTGCCTTTGCTCCTCTGTCCTGCCTCTACTCCCACCCCCACTACCTCTGGGAA $\tt TCGGCCTCTGTCCTGGAAGCCCCACCCCTTTCCTCCTGTACATAATGTCACTGGCTTGTTGGGATTTTTAATTTA$ TCTTCACTCAGCACCAAGGGCCCCCGACACTCCACTCCTGCTGCCCCTGAGCTGAGCAGAGTCATTATTGGAGAG

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

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Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242, 390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579, 576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877, 905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCCGTCACTGCG $ext{TCCTGGCTCCGGCTCCCGGCCGGCC}$ TGCCCGCGCTGGCCCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG AGCCGGACCCGCAGCACCCGGCCCCCCCGCCGGCGAGCCTGGCTACAGCTGCACCTGCCCCGGCGGGATCTCCGGCG CCAACTGCCAGCTTGTTGCAGATCCTTGTGCCAGCAACCCTTGTCACCATGGCAACTGCAGCAGCAGCAGCAGCA GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACTTCCCAGTC TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCCTGCTACTCAGGAGCCTGACA AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCGGCAAGATGCCACTGCCTCACTGATTTTGC TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT CAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACG CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTG AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCT $\tt GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTTGCCTTCCTGGTTATACTGGAGAGCTTT$ GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT ${\tt GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA}$ ACAAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCCGCTCCAT ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA CAAACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTTGCCGCA TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACTGCCGCAGCATCGACAGCG GAAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTTCTGAGTAGAGTTAGGAAAACCAC GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTCGTTTTGTGGAAA TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCTGATTGAATTTGAATCTATATTT TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC **AAGTCA**

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

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GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
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DSDGLNGTCICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

Signal sequnce.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365, 375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209, 373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466, 491-503, 529-541, 567-579, 605-617

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
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CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
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GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTTGCCTTCC
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<MW: 47787, pI: 6.11, NX(S/T): 5

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TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
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DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC AACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCCTGGAG CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCGCTACCTGACGCTC ACCCACACCTGCAACACCCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA CAACATCAGCGGGCTGACTGTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA ${\tt TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTCACAG}$ GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCCGGCAAATT CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG GCTGGAGTGAGGAAGAGCTTCAGGGTGTCCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA GTGGAAAAGGTACAGGAAGAAACAAATGGCAAAGCCCCTTGGAGGACAAGTTCCCGGATGA GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT CAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA GTCTCAGAGTCCTCCCCCCCCCCCCACCAAAACTCACACATGCCCACCGTGCCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC

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><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

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TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
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SVFLFPPKPKDT

CGCCCAGCGACGTGCGGGCGGCCTGGCCCGCGCCCTCCCGCGCCCTGCGTCCCGCGCC CTGCGCCACCGCCGAGCCGCAGCCCGCGCGCGCCCCCGGCAGCGCCCCATGCCC GCTGCTGCTCTGCGTCCTCGGGGCCCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCA ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC TGGATGTGGTGACCACGGACCCCCCCCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAG GACCAGCTGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAA ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA ACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC GGGGCGGAGAGCCGAGCTCGGGGCCGGTGCGGCGCGAGCTCAAGCAGTTCCTGGGCTGCCTC AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA $\tt CGGCGAGAGGTCCTGCCAGA{\color{red}{\bf TAA}}GCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA$ CGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC ${\tt CCTCAGCAGGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT}$ $\tt CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC$

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

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LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG
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Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site. amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224, 300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2. amino acids 325-331

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC $\tt CTGCTTCTCCCGTTACTGATCGTCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCCTAA$ GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA GGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG TCTGTGTCCTAATTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA $\mathtt{AAGCGCAA}$ \mathtt{TAA} $\mathtt{GCACCTAGTTTTCTGAAAACTGATTTACCAGGTTTAGGTTGATGTCATCTA$ ATAGTGCCAGAATTTTAATGTTTGAACTTCTGTTTTTTTCTAATTATCCCCCATTTCTTCAATA ${\tt TCATTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT}$ ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAAATGAAGAAAAAGAA CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTTGT TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG АААААААААААААААААААААААААААААААА

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<MW: 32964, pI: 9.52, NX(S/T): 1

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Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites. amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

GACTAGTTCTCTTGGAGTCTGGGAGGAGGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG GGGTGACGGCAGGGCAGGGGCCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGACT $\tt GCGAGAGGACCCCGGCGTCCCGGGCTCCCGGTGCCAGCGCT{\color{red}\underline{\textbf{ATG}}} AGGCCACTCCTCGTCCTGC$ TGCTCCTGGGCCTGGCCGGCCCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG CGATGGCCGCGACGGCCGCGCGCGCCCCGGGGCTCCGGGAGAAAAGGCGAGGGCGGGA GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGGCCGCGAGGAGAGGCGGGACCCGCGGGG CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGAAACG AGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA ${\tt CTGGCACAGCTCCCAGTCTTTGCT} \underline{{\tt TAG}} {\tt TGCCCACTGCAAAGTGAGCTCATGCTCACTCC}$ TAGAAGGAGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATT GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA ${\tt GAGGAGTGTGCTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT}$ GGGGTGCTCTCTGGTCCTCTGCTTCTCTGGATCCTCCCACCCCCTCCTGCTCCTGGG AAAAAAAAAAA

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Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCC**AT** $\underline{\mathbf{G}}$ CTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG GCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA GCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG CCAGGGCAGCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTG CAAGTGGGCTGGAACATGCAGCTGCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAA CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC AGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAG TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGC CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCT CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCA GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC $\texttt{CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCC} \underline{\textbf{T}}$ \underline{GA} GGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGCCAGGGAGGCCAGTGAGGGCCAGGGAGTG AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA TGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGAC CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAG CTGAAAAAAAAAAAAAA

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TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293, 288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

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KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
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Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAA TCCCAACAGGCAGACCATTTATTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT ${\tt TGCTGAATTTTCTAGCAGTGAACTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA}$ GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG AGCACCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTCATCAATAACCTAAACAAA ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA CCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGCCCAT GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA ${\tt GGACAGAACAACTCCGAAGAAAAGAAGAGTACTTCATC}$ GAGGTGTCCAACTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

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KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310, 430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408, 411-417, 427-433, 428-432

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Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

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Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

CACTTTCTCCCTCTCTTTCCTTTACTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC CCGCCCCCCACCCTCCTCTTCTGCACTGCCGTCCTCCGGAAGACCTTTTCCCCCTGCTCTGTT TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA CCCAAAGGGCAGAAGGGCTCCATGGGGGGCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTCACCGGCAAGTTCTACTGCTAC GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG ${\tt TGGCTACCTGGTCAAGCACGCCACCGAGCCC} \underline{{\tt TAG}} {\tt CTGGCCGGCCACCTCCTTTCCTCTCGCC}$ ACCTTCCACCCTGCGCTGTGCTGACCCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC ${\tt CCTGGCTTTGGCATTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCCC}$ CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC GAGACGCGGGTGCGGCAGGGCTCCCAGGGTGCGCACCGCGCTCCAGTCCTTGGAAATA ATTAGGCAAATTCTAAAGGTCTCAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGGCAGG AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACTTTCTTGAGGGATAGGTGGACC GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC ${\tt TTCTGTGCCGCCTCCCACACAAATCAGCCCCAGAAGGCCCCGGGGCCTTGGCTTCTGTTTTT}$ TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT CCACGTGTGTTGTTGGTTGGCAGCAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCCTTCAGAGCAGGGGAGAG $\tt CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG$ AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCACTCTCAGGAGC TGGGTGGCAGGAGAGGCAATAGCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCCAGACTCTGATCTCCAGGAACCCC ATAGCCCCTCTCCACCTCACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCC CCCAAACCCCCGCTGCCTCTTCCTTCCCCCCCATCCCCACCTGGTTTTGACTAATCCTGC TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGCGGATTCGCCGGTCCTTCCCGCGG GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCTCTCGACGCCA GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAĠAGGGAGGATTAT CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG CCAAGAGTTACCCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAA TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC ${\tt TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC}$ AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA AACCATACCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTA $\tt CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGT$ AGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTTGGTGTCCTGTTCCTGGTGATAGGCC TCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT ${\tt TATTTGATCAATGGGATCTATGTGGACATC} \underline{{\tt TAA}}{\tt GGATGGAACTCGGTGTCTCTTAATTCATT}$ TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG GCTCTGTTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC $\tt CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA$ ${\tt CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG}$ GTCTCAAACTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAAACAAAGCTCT ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAAATTCAACTGGCTTTTATGCAAA GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCTTGGTTCCAGATAAAATCAAC TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTTATATGGATTCCTTTAAAAACTTATT CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410</pre>

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

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SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

 $\tt GCGGCACCTGGAAG\underline{\textbf{ATG}} \tt CGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC$ GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACTGGGA ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACTCCCTTCCGAAATT GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACCACGGGGTCCTGAGTAAAT GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA GCCCATATTTGATGAGTATTTTGGGTTTGTTGTAAACCAATGAACATTTGCTAGTTGTATCA AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA AACTAAAATGAATGGAAATTCTTAAAAAAAAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125